SEQUENCE LISTING

<110> Dumas, Renaud
     Lebrun, Marc-Henri
     Zundel, Jean-Luc
     Effantin, Géraldine
     Morin, Valérie

<120> Use of inhibitors of ketol-acid reductoisomerase to prevent or treat fungal infection of plants

<130> A36156-PCT-USA-A 072667.0196

<140>
<141>

<160> 18

<170> Custom

<210> 1
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<212> PRT
<213> Magnaporthe grisea

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<222> (1)..(51)
<223> Putative mitochondrial transit peptide

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Leu Ala Thr Pro Ala Val Gln Arg Arg Ser Phe Val Ala Ala Ser Ser
            20   25   30

Met Val Arg Ala Thr Arg Lys Ala Ala Val Ala Pro Thr Gln Gln Gln
        35   40   45

Ile Arg Gly Val Lys Thr Met Asp Phe Ala Gly His Lys Glu Gln Val
    50   55   60

Trp Glu Arg Ala Asp Trp Pro Lys Glu Lys Leu Leu Glu Tyr Phe Lys
 65   70   75   80

Asp Asp Thr Leu Ala Leu Ile Gly Tyr Gly Ser Gln Gly His Gly Gln
                85   90   95

Gly Leu Asn Leu Arg Asp Asn Gly Leu Asn Val Ile Ile Gly Val Arg
            100   105   110

Lys Asp Gly Lys Ser Trp Lys Asp Ala Val Gln Asp Gly Trp Val Pro
            115   120   125

Gly Lys Asn Leu Phe Glu Val Asp Glu Ala Ile Ser Arg Gly Thr Val
    130   135   140

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Ile Met Asn Leu Leu Ser Asp Ala Ala Gln Ser Glu Thr Trp Pro Ala
145                 150                 155                 160

Leu Lys Pro Gln Ile Thr Lys Gly Lys Thr Leu Tyr Phe Ser His Gly
                165                 170                 175

Phe Ser Pro Val Phe Lys Asp Leu Thr Lys Val Glu Val Pro Thr Asp
                180                 185                 190

Val Asp Val Ile Leu Cys Ala Pro Lys Gly Ser Gly Arg Thr Val Arg
                195                 200                 205

Ser Leu Phe Arg Glu Gly Arg Gly Ile Asn Ser Ser Phe Ala Val Tyr
    210                 215                 220

Gln Asp Val Thr Gly Glu Ala Glu Glu Lys Ala Ile Ala Leu Gly Val
225                 230                 235                 240

Ala Ile Gly Ser Gly Tyr Leu Tyr Lys Thr Thr Phe Glu Lys Glu Val
                245                 250                 255

Tyr Ser Asp Leu Tyr Gly Glu Arg Gly Cys Leu Met Gly Gly Ile His
                260                 265                 270

Gly Met Phe Leu Ala Gln Tyr Glu Val Leu Arg Glu Arg Gly His Ser
                275                 280                 285

Pro Ser Glu Ala Phe Asn Glu Thr Val Glu Glu Ala Thr Gln Ser Leu
    290                 295                 300

Tyr Pro Leu Ile Gly Ala Asn Gly Met Asp Trp Met Tyr Glu Ala Cys
305                 310                 315                 320

Ser Thr Thr Ala Arg Arg Gly Ala Ile Asp Trp Ser Pro Arg Phe Lys
                325                 330                 335

Asp Ala Leu Lys Pro Val Phe Asn Gln Leu Tyr Asp Ser Val Lys Asp
                340                 345                 350

Gly Ser Glu Thr Gln Arg Ser Leu Asp Tyr Asn Ser Gln Pro Asp Tyr
                355                 360                 365

Arg Glu Lys Tyr Glu Ala Glu Met Glu Glu Ile Arg Asn Leu Glu Ile
    370                 375                 380

Trp Arg Ala Gly Lys Ala Val Arg Ser Leu Arg Pro Glu Asn Gln Lys
385                 390                 395                 400

Gln Lys
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<223> mitochondrial transit peptide

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<309> 1993-09-12

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Thr Ala Lys Arg Thr Phe Ala Leu Ala Thr Arg Ala Ala Ala Tyr Ser
             20   25   30

Arg Pro Ala Ala Arg Phe Val Lys Pro Met Ile Thr Thr Arg Gly Leu
         35   40   45

Lys Gln Ile Asn Phe Gly Gly Thr Val Glu Thr Val Tyr Glu Arg Ala
     50   55   60

Asp Trp Pro Arg Glu Lys Leu Leu Asp Tyr Phe Lys Asn Asp Thr Phe
65   70   75   80

Ala Leu Ile Gly Tyr Gly Ser Gln Gly Tyr Gly Gln Gly Leu Asn Leu
             85   90   95

Arg Asp Asn Gly Leu Asn Val Ile Ile Gly Val Arg Lys Asp Gly Ala
         100   105   110

Ser Trp Lys Ala Ala Ile Glu Asp Gly Trp Val Pro Gly Lys Asn Leu
         115   120   125

Phe Thr Val Glu Asp Ala Ile Lys Arg Gly Ser Tyr Val Met Asn Leu
     130   135   140

Leu Ser Asp Ala Ala Gln Ser Glu Thr Trp Pro Ala Ile Lys Pro Leu
145   150   155   160

Leu Thr Lys Gly Lys Thr Leu Tyr Phe Ser His Gly Phe Ser Pro Val
             165   170   175

Phe Lys Asp Leu Thr His Val Glu Pro Pro Lys Asp Leu Asp Val Ile
             180   185   190

Leu Val Ala Pro Lys Gly Ser Gly Arg Thr Val Arg Ser Leu Phe Lys
         195   200   205

Glu Gly Arg Gly Ile Asn Ser Ser Tyr Ala Val Trp Asn Asp Val Thr
     210   215   220

Gly Lys Ala His Glu Lys Ala Gln Ala Leu Ala Val Ala Ile Gly Ser
225   230   235   240

Gly Tyr Val Tyr Gln Thr Thr Phe Glu Arg Glu Val Asn Ser Asp Leu
                245   250   255

Tyr Gly Glu Arg Gly Cys Leu Met Gly Gly Ile His Gly Met Phe Leu
                260   265   270

Ala Gln Tyr Asp Val Leu Arg Glu Asn Gly His Ser Pro Ser Glu Ala
                275   280   285

Phe Asn Glu Thr Val Glu Glu Ala Thr Gln Ser Leu Tyr Pro Leu Ile
    290   295   300

Gly Lys Tyr Gly Met Asp Tyr Met Tyr Asp Ala Cys Ser Thr Thr Ala
305   310   315   320

Arg Arg Gly Ala Leu Asp Trp Tyr Pro Ile Phe Lys Asn Ala Leu Lys
                325   330   335

Pro Val Phe Gln Asp Leu Tyr Glu Ser Thr Lys Asn Gly Thr Glu Thr
                340   345   350

Lys Arg Ser Leu Glu Phe Asn Ser Gln Pro Asp Tyr Arg Glu Lys Leu
                355   360   365

Glu Lys Glu Leu Asp Thr Ile Arg Asn Met Glu Ile Trp Lys Val Gly
    370   375   380

Lys Glu Val Arg Lys Leu Arg Pro Glu Asn Gln
385   390   395

<210> 3
<211> 400
<212> PRT
<213> Neurospora crassa

<220>
<221> TRANSIT
<222> (1)..(53)
<223> putative mitochondrial transit peptide

<300>
<308> gb:M84189.1
<309> 1996-05-23

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Met Ala Ala Arg Asn Cys Thr Lys Ala Leu Arg Pro Leu Ala Arg Gln
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Leu Ala Thr Pro Ala Val Gln Arg Arg Thr Phe Val Ala Ala Ala Ser
                20   25   30

Ala Val Arg Ala Ser Val Ala Val Lys Ala Val Ala Ala Pro Ala Arg
            35   40   45

Gln Gln Val Arg Gly Val Lys Thr Met Asp Phe Ala Gly His Lys Glu
    50   55   60

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Glu Val His Glu Arg Ala Asp Trp Pro Ala Glu Lys Leu Leu Asp Tyr
 65                      70                  75                      80

Phe Lys Asn Asp Thr Leu Ala Leu Ile Gly Tyr Gly Ser Gln Gly His
                    85                  90                  95

Gly Gln Gly Leu Asn Leu Arg Asp Asn Gly Leu Asn Val Ile Val Gly
            100                 105                 110

Val Arg Lys Asn Gly Lys Ser Trp Glu Asp Ala Ile Gln Asp Gly Trp
            115                 120                 125

Val Pro Gly Lys Asn Leu Phe Asp Val Asp Glu Ala Ile Ser Arg Gly
            130                 135                 140

Thr Ile Val Met Asn Leu Leu Ser Asp Ala Ala Gln Ser Glu Thr Trp
145                 150                 155                 160

Pro His Ile Lys Pro Gln Ile Thr Lys Gly Lys Thr Leu Tyr Phe Ser
                165                 170                 175

His Gly Phe Ser Pro Val Phe Lys Asp Leu Thr Lys Val Glu Val Pro
            180                 185                 190

Thr Asp Val Asp Val Ile Leu Val Ala Pro Lys Gly Ser Gly Arg Thr
            195                 200                 205

Val Arg Ser Leu Phe Arg Glu Gly Arg Gly Ile Asn Ser Ser Phe Ala
    210                 215                 220

Val Tyr Gln Asp Val Thr Gly Lys Ala Lys Glu Lys Ala Val Ala Leu
225                 230                 235                 240

Gly Val Ala Val Gly Ser Gly Tyr Leu Tyr Glu Thr Thr Phe Glu Lys
            245                 250                 255

Glu Val Tyr Ser Asp Leu Tyr Gly Glu Arg Gly Cys Leu Met Gly Gly
            260                 265                 270

Ile His Gly Met Phe Leu Ala Gln Tyr Glu Val Leu Arg Glu Arg Gly
            275                 280                 285

His Ser Pro Ser Glu Ala Phe Asn Glu Thr Val Glu Glu Ala Thr Gln
    290                 295                 300

Ser Leu Tyr Pro Leu Ile Gly Ala His Gly Met Asp Trp Met Phe Asp
305                 310                 315                 320

Ala Cys Ser Thr Thr Ala Arg Arg Gly Ala Ile Asp Trp Thr Pro Lys
            325                 330                 335

Phe Lys Asp Ala Leu Lys Pro Val Phe Asn Asn Leu Tyr Asp Ser Val
            340                 345                 350

Lys Asn Gly Asp Glu Arg Lys Arg Ser Leu Glu Tyr Asn Ser Gln Pro
    355                 360                 365
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Asp Tyr Arg Glu Arg Tyr Glu Ala Glu Leu Asp Glu Ile Arg Asn Leu
    370   375   380

Glu Ile Trp Arg Ala Gly Lys Arg Ser Leu Arg Pro Glu Asn Gln Lys
385   390   395   400

<210> 4
<211> 1356
<212> DNA
<213> Magnaporthe grisea

<220>
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<222> (1)..(43)

<220>
<221> CDS
<222> (44)..(1246)

<220>
<221> 3'UTR
<222> (1247)..(1356)

<220>
<221> polyA_site
<222> (1322)..(1330)

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ttgttttct tggttcctta ttctaccttg tcacacaaca aac atg tct gct cgc   55
                                                Met Ser Ala Arg
                                                  1

ggt ttc tca aag gct ttg agg cca atg gcc cgc caa ttg gcc act ccc   103
Gly Phe Ser Lys Ala Leu Arg Pro Met Ala Arg Gln Leu Ala Thr Pro
  5   10   15   20

gcc gtt cag agg cgt acc ttc gtg gct gct tct agc atg gtg cgg gcc   151
Ala Val Gln Arg Arg Thr Phe Val Ala Ala Ser Ser Met Val Arg Ala
                 25   30   35

acc agg aaa gcc gcc gtc gct ccc act cag cag cag atc cgt ggt gtc   199
Thr Arg Lys Ala Ala Val Ala Pro Thr Gln Gln Gln Ile Arg Gly Val
             40   45   50

aag acc atg gat ttt gct ggc cac aag gag cag gtc tgg gag cgt gcc   247
Lys Thr Met Asp Phe Ala Gly His Lys Glu Gln Val Trp Glu Arg Ala
             55   60   65

gac tgg ccc aag gag aag ctg ctg gag tac ttc aag gac gac acc ctt   295
Asp Trp Pro Lys Glu Lys Leu Leu Glu Tyr Phe Lys Asp Asp Thr Leu
         70   75   80

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gcc ctc atc ggc tat ggt tcg cag ggc cac ggc cag ggt ctt aac ctc      343
Ala Leu Ile Gly Tyr Gly Ser Gln Gly His Gly Gln Gly Leu Asn Leu
 85                  90                  95                 100

cgc gac aac ggc ctc aac gtc atc atc ggt gtg cgc aag gac gga aag      391
Arg Asp Asn Gly Leu Asn Val Ile Ile Gly Val Arg Lys Asp Gly Lys
                    105                 110                 115

tcg tgg aag gac gcc gtc cag gac ggc tgg gtt ccc ggc aag aac ctc      439
Ser Trp Lys Asp Ala Val Gln Asp Gly Trp Val Pro Gly Lys Asn Leu
                120                 125                 130

ttc gag gtc gac gag gcc atc tcg cgc ggt acc gtc atc atg aac ctt      487
Phe Glu Val Asp Glu Ala Ile Ser Arg Gly Thr Val Ile Met Asn Leu
            135                 140                 145

ctg agc gac gct gcc cag agc gag acg tgg cct gct ctg aag ccc cag      535
Leu Ser Asp Ala Ala Gln Ser Glu Thr Trp Pro Ala Leu Lys Pro Gln
        150                 155                 160

atc act aag ggc aag act ctc tac ttc tcg cac ggt ttc tct ccc gtc      583
Ile Thr Lys Gly Lys Thr Leu Tyr Phe Ser His Gly Phe Ser Pro Val
165                 170                 175                 180

ttc aag gac ctc acc aag gtc gag gtc ccc acc gac gtc gac gtc atc      631
Phe Lys Asp Leu Thr Lys Val Glu Val Pro Thr Asp Val Asp Val Ile
                185.                190                 195

ctc tgc gcc ccc aag ggc tcc ggc cgc act gtc cgc tcg ctc ttc cgc      679
Leu Cys Ala Pro Lys Gly Ser Gly Arg Thr Val Arg Ser Leu Phe Arg
                200                 205                 210

gag ggt cgt ggc atc aac tcc tcc ttc gcc gtc tac cag gac gtg act      727
Glu Gly Arg Gly Ile Asn Ser Ser Phe Ala Val Tyr Gln Asp Val Thr
            215                 220                 225

ggc gag gct gaa gag aag gct atc gct ctc ggt gtt gcc att ggc agt      775
Gly Glu Ala Glu Glu Lys Ala Ile Ala Leu Gly Val Ala Ile Gly Ser
        230                 235                 240

ggt tac ctc tac aag acc acc ttc gag aag gag gtc tac tct gac ctg      823
Gly Tyr Leu Tyr Lys Thr Thr Phe Glu Lys Glu Val Tyr Ser Asp Leu
245                 250                 255                 260

tac ggt gag cgt ggc tgc ctg atg ggt ggt atc cac ggt atg ttc ctt      871
Tyr Gly Glu Arg Gly Cys Leu Met Gly Gly Ile His Gly Met Phe Leu
                265                 270                 275

gcc cag tac gag gtt ctc cgc gag cgt ggc cac agc ccc tcg gag gct      919
Ala Gln Tyr Glu Val Leu Arg Glu Arg Gly His Ser Pro Ser Glu Ala
                280                 285                 290

ttc aac gag act gtc gag gag gcc acc cag tct ctc tac ccc ctg atc      967
Phe Asn Glu Thr Val Glu Glu Ala Thr Gln Ser Leu Tyr Pro Leu Ile
            295                 300                 305

ggt gcc aac ggc atg gac tgg atg tac gag gcc tgc tct acc act gct     1015
Gly Ala Asn Gly Met Asp Trp Met Tyr Glu Ala Cys Ser Thr Thr Ala
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Gly Ala Asn Gly Met Asp Trp Met Tyr Glu Ala Cys Ser Thr Thr Ala
    310                 315                 320

cgt cgt ggt gcc att gac tgg agc ccc cgc ttc aag gac gcc ctc aag   1063
Arg Arg Gly Ala Ile Asp Trp Ser Pro Arg Phe Lys Asp Ala Leu Lys
325             330                 335                 340

ccc gtc ttc aac cag ctc tac gac tcg gtc aag gac ggc tct gag act   1111
Pro Val Phe Asn Gln Leu Tyr Asp Ser Val Lys Asp Gly Ser Glu Thr
                345                 350                 355

cag cgc tcg ctc gac tac aac agc cag ccc gac tac cgc gag aag tac   1159
Gln Arg Ser Leu Asp Tyr Asn Ser Gln Pro Asp Tyr Arg Glu Lys Tyr
            360                 365                 370

gag gcc gag atg gag gag atc cgc aac ctg gag atc tgg agg gcg ggt   1207
Glu Ala Glu Met Glu Glu Ile Arg Asn Leu Glu Ile Trp Arg Ala Gly
        375                 380                 385

aag gct gtg cgc agc ctc cgt cct gag aac cag aag taa actgtatatt   1256
Lys Ala Val Arg Ser Leu Arg Pro Glu Asn Gln Lys
    390                 395                 400

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ttgttgaaaa ataatctgga gtcatcgcta catttcttgg                      1356


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<212> PRT
<213> Magnaporthe grisea

<400> 5
Met Ser Ala Arg Gly Phe Ser Lys Ala Leu Arg Pro Met Ala Arg Gln
 1           5                  10                  15
Leu Ala Thr Pro Ala Val Gln Arg Arg Thr Phe Val Ala Ala Ser Ser
            20                  25                  30
Met Val Arg Ala Thr Arg Lys Ala Ala Val Ala Pro Thr Gln Gln Gln
        35                  40                  45
Ile Arg Gly Val Lys Thr Met Asp Phe Ala Gly His Lys Glu Gln Val
    50                  55                  60
Trp Glu Arg Ala Asp Trp Pro Lys Glu Lys Leu Leu Glu Tyr Phe Lys
65                  70                  75                  80

Asp Asp Thr Leu Ala Leu Ile Gly Tyr Gly Ser Gln Gly His Gly Gln
                85                  90                  95
Gly Leu Asn Leu Arg Asp Asn Gly Leu Asn Val Ile Ile Gly Val Arg
            100                 105                 110
Lys Asp Gly Lys Ser Trp Lys Asp Ala Val Gln Asp Gly Trp Val Pro
            115                 120                 125
Gly Lys Asn Leu Phe Glu Val Asp Glu Ala Ile Ser Arg Gly Thr Val
    130                 135                 140
Ile Met Asn Leu Leu Ser Asp Ala Ala Gln Ser Glu Thr Trp Pro Ala
145                 150                 155                 160
Leu Lys Pro Gln Ile Thr Lys Gly Lys Thr Leu Tyr Phe Ser His Gly
                165                 170                 175
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Phe Ser Pro Val Phe Lys Asp Leu Thr Lys Val Glu Val Pro Thr Asp
        180                 185                 190
Val Asp Val Ile Leu Cys Ala Pro Lys Gly Ser Gly Arg Thr Val Arg
        195                 200                 205
Ser Leu Phe Arg Glu Gly Arg Gly Ile Asn Ser Ser Phe Ala Val Tyr
    210                 215                 220
Gln Asp Val Thr Gly Glu Ala Glu Glu Lys Ala Ile Ala Leu Gly Val
225                 230                 235                 240
Ala Ile Gly Ser Gly Tyr Leu Tyr Lys Thr Thr Phe Glu Lys Glu Val
                245                 250                 255
Tyr Ser Asp Leu Tyr Gly Glu Arg Gly Cys Leu Met Gly Gly Ile His
            260                 265                 270
Gly Met Phe Leu Ala Gln Tyr Glu Val Leu Arg Glu Arg Gly His Ser
        275                 280                 285
Pro Ser Glu Ala Phe Asn Glu Thr Val Glu Glu Ala Thr Gln Ser Leu
    290                 295                 300
Tyr Pro Leu Ile Gly Ala Asn Gly Met Asp Trp Met Tyr Glu Ala Cys
305                 310                 315                 320
Ser Thr Thr Ala Arg Arg Gly Ala Ile Asp Trp Ser Pro Arg Phe Lys
                325                 330                 335
Asp Ala Leu Lys Pro Val Phe Asn Gln Leu Tyr Asp Ser Val Lys Asp
            340                 345                 350
Gly Ser Glu Thr Gln Arg Ser Leu Asp Tyr Asn Ser Gln Pro Asp Tyr
            355                 360                 365
Arg Glu Lys Tyr Glu Ala Glu Met Glu Glu Ile Arg Asn Leu Glu Ile
    370                 375                 380
Trp Arg Ala Gly Lys Ala Val Arg Ser Leu Arg Pro Glu Asn Gln Lys
385                 390                 395                 400
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<211> 3827
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<213> Magnaporthe grisea

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<222> (1700)..(1781)

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<222> (2952)..(3061)

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agatccgcaa cctggagatc tggagggcgg gtaaggctgt gcgcagcctc cgtcctgaga 2940

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accagaagta aactgtatat ttgcttccaa gttccggtca aatgccagtg gatctctaca 3000
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<210> 7
<211> 20
<212> DNA
<213> Artificial sequence

<220>
<223> Description of the artificial sequence: primer 1

<400> 7
gaytayttya araaygayac                                        20


<210> 8
<211> 20
<212> DNA
<213> Artificial sequence

<220>
<223> Description of the artificial sequence: primer 2

<400> 8
atgttyytng cncartayga                                        20


<210> 9
<211> 20
<212> DNA
<213> Artificial sequence

<220>
<223> Description of the artificial sequence: primer 3

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gayggntggg tnccnggnaa                                        20


<210> 10
<211> 21
<212> DNA
<213> Artificial sequence
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<220>
<223> Description of the artificial sequence: primer 4

<400> 10
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<210> 11
<211> 29
<212> DNA
<213> Artificial sequence

<220>
<223> Description of the artificial sequence: primer 2'

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ctgcttccat ggcaccagct gcccgtttc   29

<210> 12
<211> 29
<212> DNA
<213> Artificial sequence

<220>
<223> Description of the artificial sequence: primer 1'

<400> 12
ctaccccat ggtgaagcaa atcaacttc   29

<210> 13
<211> 36
<212> DNA
<213> Artificial sequence

<220>
<223> Description of the artificial sequence: primer 3'

<400> 13
gcacttgata ttattgtcga ctttattggt tttctg   36

<210> 14
<211> 20
<212> DNA
<213> Artificial sequence

<220>
<223> Description of the artificial sequence: primer
     13U

<400> 14
aacgacaccc ttgccctcat   20

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<210> 15
<211> 20
<212> DNA
<213> Artificial sequence

<220>
<223> Description of the artificial sequence: primer
      300U

<400> 15
accgtttctt tttacttacc                                              20


<210> 16
<211> 20
<212> DNA
<213> Artificial sequence

<220>
<223> Description of the artificial sequence: primer
      549L

<400> 16
gcgatagcct tctcttcagc                                              20


<210> 17
<211> 20
<212> DNA
<213> Artificial sequence

<220>
<223> Description of the artificial sequence: primer
      22U

<400> 17
ttgtttttct tggttcctta                                              20


<210> 18
<211> 20
<212> DNA
<213> Artificial sequence

<220>
<223> Description of the artificial sequence: Primer
      1603L

<400> 18
ccaagaaatg tagcgatgac                                              20
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